SEQUENCE LISTING

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Yao, Yue

<120> UMLR POLYPEPTIDES

<130> 99-75

<140> 09/695,369
<141> 2000-10-23

<150> 60/160, 880
<151> 1999-10-22

<150> 60/163, 215
<151> 1999-11-02

<150> 60/218,769
<151> 2000-07-17

<150> 60/222,221
<151> 2000-08-01

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gggagcaaga gccatctact cgtccgttac cggccttccc acc atg gat tgc caa         115
                                                Met Asp Cys Gln
                                                 1

gaa aat gag tac tgg gac caa tgg gga cgg tgt gtc acc tgc caa cgg         163
Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val Thr Cys Gln Arg
 5                  10                  15                  20

tgt ggt cct gga cag gag cta tcc aag gat tgt ggt tat gga gag ggt         211
Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly Tyr Gly Glu Gly
                25                  30                  35

gga gat gcc tac tgc aca gcc tgc cct cct cgc agg tac aaa agc agc         259
Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg Tyr Lys Ser Ser
            40                  45                  50

tgg ggc cac cac aaa tgt cag agt tgc atc acc tgt gct gtc atc aat         307
Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys Ala Val Ile Asn
        55                  60                  65

cgt gtt cag aag gtc aac tgc aca gct acc tct aat gct gtc tgt ggg         355
Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn Ala Val Cys Gly
    70                  75                  80

gac tgt ttg ccc agg ttc tac cga aag aca cgc att gga ggc ctg cag         403
Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile Gly Gly Leu Gln
 85                  90                  95                  100

gac caa gag tgc atc ccg tgc acg aag cag acc ccc acc tct gag gtt         451
Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro Thr Ser Glu Val
                105                 110                 115

caa tgt gcc ttc cag ttg agc tta gtg gag gca gat gca ccc aca gtg         499
Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala Pro Thr Val
            120                 125                 130

ccc cct cag gag gcc aca ctt gtt gca ctg gtg agc agc ctg cta gtg         547
Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser Leu Leu Val
        135                 140                 145
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gtg ttt acc ctg gcc ttc ctg ggg ctc ttc ttc ctc tac tgc aag cag      595
Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr Cys Lys Gln
    150                 155                 160

ttc ttc aac aga cat tgc cag cgt gga ggt ttg ctg cag ttt gag gct      643
Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu Gln Phe Glu Ala
165                 170                 175                 180

gat aaa aca gca aag gag gaa tct ctc ttc ccc gtg cca ccc agc aag      691
Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val Pro Pro Ser Lys
                185                 190                 195

gag acc agt gct gag tcc caa gag tcc ttt acc atg gcc tcc tgc acc      739
Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
            200                 205                 210

tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca gag      787
Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
        215                 220                 225

ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct gag      835
Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
    230                 235                 240

acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg gag ctc      883
Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
245                 250                 255                 260

aat gtg ccc ttt gaa gtt ccc agc cct taa ctctaatgag gtctcttggg        933
Asn Val Pro Phe Glu Val Pro Ser Pro  *
                265
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cccctggcag ccttgcccag ttgttctctc tggactctgt tcctatacca caacagcagc    993
aggggcctga aatgtgatgt ccacaagagc taatacccta cagatggggc atatcctatc   1053
ccatcccacc agaggattga ttctccattt cacaaggact gatctggagc atttcttgct   1113
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<210> 2
<211> 269
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<213> Homo sapiens

<400> 2

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            20                  25                  30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
                85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
            100                 105                 110
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
        115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
    130                 135                 140
Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145                 150                 155                 160
Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
                165                 170                 175
Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
            180                 185                 190
Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met
        195                 200                 205
Ala Ser Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile
    210                 215                 220
Glu Cys Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr
225                 230                 235                 240
Thr Gly Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp
                245                 250                 255
Arg Leu Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
            260                 265
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<223> n = A,T,C or G

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tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn 180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay 240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytncar 300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty 360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn 420
gcnytngtnw snwsnytnyt ngtngtntty acnytngcnt tyytnggnyt nttyttyytn 480
taytgyaarc arttyttyaa ymgncaytgy carmgnggng gnytnytnca rttygargcn 540
gayaaracng cnaargarga rwsnytntty ccngtnccnc cnwsnaarga racnwsngcn 600
garwsncarg arwsnttyac natggcnwsn tgyacnwsng arwsncayws ncaytgggtn 660
caywsnccna thgartgyac ngarytngay ytncaraart tywsnwsnws ngcnwsntay 720
acnggngcng aracnytngg nggnaayacn gtngarwsna cnggngaymg nytngarytn 780
aaygtnccnt tygargtncc nwsnccn 807

<210> 4
<211> 41
<212> PRT
<213> Artificial Sequence

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<223> Pseudo repeat motif #1

<221> VARIANT
<222> (1)...(1)
<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(12)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (13)...(16)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (19)...(20)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (22)...(26)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (27)...(30)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (32)...(37)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (38)...(39)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (41)...(41)
<223> Xaa is any amino acid residue

<400> 4

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Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                  10                  15
Cys Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35                  40
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<210> 5
<211> 45
<212> PRT
<213> Artificial Sequence

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<223> Pseudo repeat motif #2

<221> VARIANT
<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(15)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (16)...(17)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (19)...(20)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (22)...(23)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (24)...(24)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (26)...(33)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (34)...(36)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (38)...(44)
<223> Each Xaa is independently any amino acid residue

<400> 5

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Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                  10                  15
Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
```

Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
35 40 45

<210> 6
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #3

<221> VARIANT
<222> (1)...(1)
<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(7)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (8)...(8)
<223> Xaa is any amino acid residue or not present

<221> VARIANT
<222> (9)...(14)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (15)...(18)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (20)...(21)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (23)...(24)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (25)...(29)
<223> Each Xaa is independently any amino acid residue

or not present

<221> VARIANT
<222> (31)...(38)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (39)...(39)
<223> Xaa is any amino acid residue or not present

<221> VARIANT
<222> (41)...(47)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (49)...(49)
<223> Xaa is any amino acid residue or not present

<400> 6

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Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                  10                  15
Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
        35                  40                  45
Xaa
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<210> 7
<211> 48
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<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #3 alternative motif

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<221> VARIANT
<222> (3)...(7)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (8)...(8)
<223> Xaa is independently any amino acid residue or not present

<221> VARIANT
<222> (10)...(13)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (14)...(18)
<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT
<222> (20)...(21)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (23)...(24)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (25)...(29)
<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT
<222> (31)...(40)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (41)...(46)
<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT
<222> (48)...(48)
<223> Xaa is any amino acid residue

<400> 7

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Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                  10                  15
Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35                  40                  45
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<210> 8
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #4

<221> VARIANT
<222> (1)...(1)
<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(12)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (13)...(16)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (18)...(19)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (21)...(22)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (24)...(27)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (28)...(33)
<223> Each Xaa is independently any amino acid residue

or not present

<221> VARIANT
<222> (35)...(37)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (38)...(41)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (43)...(43)
<223> Each Xaa is independently any amino acid residue

<400> 8

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Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                  10                  15
Cys Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35                  40
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<210> 9
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #4 alternative motif

<221> VARIANT
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<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(12)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (13)...(16)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (18)...(22)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (24)...(27)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (28)...(33)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (34)...(37)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (38)...(41)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (43)...(43)
<223> Xaa is any amino acid residue

<400> 9

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 1               5                  10                  15
Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35                  40
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<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25352

<400> 10
ccttgcccag ttgttctc 18

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25353

<400> 11
tctggtggga tgggatag 18

<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25364

<400> 12
acctgtgctg tcatcaatcg tgttca 26

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25365

<400> 13
cccccaaggt ctcagctcca gtat 24

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25352

<400> 14
ccttgcccag ttgttctc 18

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25353

<400> 15
tctggtggga tgggatag 18

<210> 16
<211> 6
<212> PRT
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<220>
<223> Artificial Protein

<400> 16
Glu Tyr Met Pro Met Glu
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<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 17
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<220>
<223> oligonucleotide primer ZC25596

<400> 18
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<210> 19
<211> 108
<212> DNA
<213> Homo sapiens

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<223> tPA leader

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tcgctcagcc aggaaatcca tgccgagttg agacgcttcc gtagatcc 108

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<212> DNA
<213> Artificial Sequence

<220>
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ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 120
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180
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gagtacaagt gcaaggtctc caacaaagcc ctcccatcct ccatcgagaa aaccatctcc 360
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag 420
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 480
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 540
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 600
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 660
cagaagagcc tctccctgtc tccgggtaaa taa 693

<210> 21
<211> 534

<212> DNA
<213> Artficial sequence

<220>
<223> Polynucleotide Construct

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aatgagtact gggaccaatg gggacggtgt gtcacctgcc aacggtgtgg tcctggacag 180
gagctatcca aggattgtgg ttatggagag ggtggagatg cctactgcac agcctgccct 240
cctcgcaggt acaaaagcag ctggggccac cacaaatgtc agagttgcat cacctgtgct 300
gtcatcaatc gtgttcagaa ggtcaactgc acagctacct ctaatgctgt ctgtggggac 360
tgtttgccca ggttctaccg aaagacacgc attggaggcc tgcaggacca agagtgcatc 420
ccgtgcacga agcagacccc cacctctgag gttcaatgtg ccttccagtt gagcttagtg 480
gaggcagatg cacccacagt ggagcccaga tctgaatata tgcccatgga ataa 534

<210> 22
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> construct

<400> 22
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aatgagtact gggaccaatg gggacggtgt gtcacctgcc aacggtgtgg tcctggacag 180
gagctatcca aggattgtgg ttatggagag ggtggagatg cctactgcac agcctgccct 240
cctcgcaggt acaaaagcag ctggggccac cacaaatgtc agagttgcat cacctgtgct 300
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tgtttgccca ggttctaccg aaagacacgc attggaggcc tgcaggacca agagtgcatc 420
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gaggcagatg cacccacagt ggagcccaga tcttcagaca aaactcacac atgcccaccg 540
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gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 660
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 720
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 780
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tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 960
gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1020

aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1080
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1140
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<210> 23
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC26463

<400> 23
atgcattaac cctcactaaa gggccttcct ggggctcttc ttcctct 47

<210> 24
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC26464

<400> 24
taatacgact cactataggg aggggcccct gctgctgttg tggtat 46

<210> 25
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC26470

<400> 25
atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca 49

<210> 26
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC26471

<400> 26
taatacgact cactataggg aggcccccaa ggtctcagct ccagtat 47

<210> 27
<211> 297
<212> PRT
<213> Homo sapiens

<400> 27
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
1 5 10 15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
20 25 30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
35 40 45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
50 55 60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65 70 75 80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
85 90 95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
100 105 110
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
115 120 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
130 135 140
Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145 150 155 160
Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
165 170 175
Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
180 185 190
Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn Ile
195 200 205
Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser Ser
210 215 220

```
Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
225                 230                 235                 240
Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
                245                 250                 255
Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
            260                 265                 270
Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
        275                 280                 285
Asn Val Pro Phe Glu Val Pro Ser Pro
    290                 295
```

<210> 28
<211> 891
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence

<221> misc_feature
<222> (1)...(891)
<223> n = A,T,C or G

<400> 28

```
atggaytgyc argaraayga rtaytgggay cartggggnm gntgygtnac ntgycarmgn      60
tgyggnccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay     120
tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn     180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay     240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytncar     300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty     360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn     420
gcnytngtnw snwsnytnyt ngtngtntty acnytngcnt tyytnggnyt nttyttyytn     480
taytgyaarc arttyttyaa ymgncaytgy carmgnggng gnytnytnca rttygargcn     540
gayaaracng cnaargarga rwsnytntty ccngtnccnc cnwsnaarga racnwsngcn     600
garwsncarg tnwsngaraa yathttycar acncarccny tnaayccnat hytngargay     660
gaytgywsnw snacnwsngg nttyccnacn cargarwsnt tyacnatggc nwsntgyacn     720
wsngarwsnc aywsncaytg ggtncaywsn ccnathgart gyacngaryt ngayytncar     780
aarttywsnw snwsngcnws ntayacnggn gcngaracny tnggnggnaa yacngtngar     840
wsnacnggng aymgnytnga rytnaaygtn ccnttygarg tnccnwsncc n              891
```

<210> 29
<211> 267
<212> PRT

<213> Homo sapiens

<400> 29

```
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1               5                  10                  15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
            20                  25                  30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
                85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
            100                 105                 110
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
        115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Gly Gly
    130                 135                 140
Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe
145                 150                 155                 160
Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu
                165                 170                 175
Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
            180                 185                 190
Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
        195                 200                 205
Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
    210                 215                 220
Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
225                 230                 235                 240
Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
                245                 250                 255
Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
            260                 265
```

<210> 30
<211> 801
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence

<221> misc_feature
<222> (1)...(801)
<223> n = A,T,C or G

<400> 30
atggaytgyc argaraayga rtaytgggay cartggggnm gntgygtnac ntgycarmgn 60
tgyggnccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay 120
tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn 180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay 240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytncar 300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty 360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn 420
gcnytnggng gnytnytnca rttygargcn gayaaracng cnaargarga rwsnytntty 480
ccngtnccnc cnwsnaarga racnwsngcn garwsncarg tnwsngaraa yathttycar 540
acncarccny tnaayccnat hytngargay gaytgywsnw snacnwsngg nttyccnacn 600
cargarwsnt tyacnatggc nwsntgyacn wsngarwsnc aywsncaytg ggtncaywsn 660
ccnathgart gyacngaryt ngayytncar aarttywsnw snwsngcnws ntayacnggn 720
gcngaracny tnggnggnaa yacngtngar wsnacnggng aymgnytnga rytnaaygtn 780
ccnttygarg tnccnwsncc n 801

<210> 31
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(529)
<223> n = A,T,C or G

<400> 31
ggattcnatn nctgaggntg natggcnttc nagttnwgas tkagtggagg cagatgcasc 60
cacagtgccc gcctcaggag gycacacttg ttgcrmtggt gagcagcstg ctagtggtgt 120
ttrccctggc cttcctgggg ctcttcttcc tcwacygcaa gcagttcttc aacagacatt 180
gycagcsgng gaggtttgct gcagtttgag gctgatraaa cagcaaagga ggaatctstm 240
ttycycgtgc cacccagcaa ggagaccagt gctgagtccc aagtgagtga gaacatyttt 300
cakacccagm cacttaaccc tatcctyrag gacgactgca rctcgactag tggyttcccc 360
acacaggart mctttaccat ggcctyctgc acctyagaga gccactscca ctgggwccac 420
arccccatcg aatgcacaka gctggacctg caaaagtttt ccagctctgc ctcctatact 480
ggagctgara ccttgggggg aaacacagnc aaaagcactg ganacaggg 529

<210> 32
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 32
cagttgagct tagtggaggc agatgcaccc acagtgcccc ctcaggaggc cacacttgtt 60
gsactggagg tttgctgcag tttgaggctg ataaaacagc aaaggaggaa tctctcttns 120
ccgtgccacc cagcaaggag accagtgctg agtcccaagt gagtgagaac atctttcaga 180
cccagccact taaccctatc ctcgaggacg actgcagctc gactagtggc ttccccacac 240
aggagtcctt taccatggcc tcctgcacct cagagagcca ctcccactgg gtccacagcc 300
ccatcgaatg cacagagctg gacctgcaaa agttttccag ctctgcctcc tatactggag 360
ctgagacctt ggggggaaac acagtcgaaa gcactggaga c 401

<210> 33
<211> 528
<212> DNA
<213> Homo sapiens

<400> 33
ctctgaggtt caatgtgcct tccagttgag cttagtggag gcagatgcac ccacagtgcc 60
ccctcaggag gccacacttg ttgcactggt gagcagcctg ctagtggtgt ttaccctggc 120
cttcctgggg ctcttcttcc tctactgcaa gcagttcttc aacagacatt gccagcgtgt 180
tgcaggaggt ttgctgcagt ttgaggctga taaaacagca aaggaggaat ctctcttccc 240
cgtgccaccc agcaaggaga ccagtgctga gtcccaagtg agtgagaaca tctttcagac 300
ccagccactt aaccctatcc tcgaggacga ctgcagctcg actagtggct tccccacaca 360
ggagtccttt accatggcct cctgcacctc agagagccac tcccactggg tccacagccc 420
catcgaatgc acagagctgg acctgcaaaa gttttccagc tctgcctcct atactggagc 480
tgagaccttg gggggaaaca cagtcgaaag cactggagac aggctgga 528

<210> 34
<211> 175
<212> PRT
<213> Homo sapiens

<400> 34

```
Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala
 1               5                  10                  15
Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser
            20                  25                  30
Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr
        35                  40                  45
Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly Leu
    50                  55                  60
Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro
65                  70                  75                  80
Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn
                85                  90                  95
Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser
            100                 105                 110
Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys
        115                 120                 125
Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr
    130                 135                 140
Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala
145                 150                 155                 160
Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
                165                 170                 175
```

<210> 35
<211> 299
<212> PRT
<213> Homo sapiens

<400> 35

```
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1               5                  10                  15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
            20                  25                  30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
                85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
            100                 105                 110
```

```
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
        115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
    130                 135                 140
Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145                 150                 155                 160
Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly
                165                 170                 175
Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe
            180                 185                 190
Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu
        195                 200                 205
Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
    210                 215                 220
Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
225                 230                 235                 240
Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
                245                 250                 255
Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
            260                 265                 270
Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
        275                 280                 285
Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
    290                 295
```

<210> 36
<211> 431
<212> DNA
<213> Homo sapiens

<400> 36

```
ctc tga ggt tca atg tgc ctt cca gtt gag ctt agt gga ggc aga tgc       48
acc cac agt gcc ccc tca gga ggc cac act tgt tgc act gga ggt ttg       96
ctg cag ttt gag gct gat aaa aca gca aag gag gaa tct ctc ttc ccc      144
gtg cca ccc agc aag gag acc agt gct gag tcc caa gtg agt gag aac      192
atc ttt cag acc cag cca ctt aac cct atc ctc gag gac gac tgc agc      240
tcg act agt ggc ttc ccc aca cag gag tcc ttt acc atg gcc tcc tgc      288
acc tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca      336
gag ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct      384
gag acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg ga       431
```

<210> 37
<211> 142

<212> PRT
<213> Homo sapiens

<400> 37
Leu Gly Ser Met Cys Leu Pro Val Glu Leu Ser Gly Gly Arg Cys Thr
1 5 10 15
His Ser Ala Pro Ser Gly Gly His Thr Cys Cys Thr Gly Gly Leu Leu
20 25 30
Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
35 40 45
Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn Ile
50 55 60
Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser Ser
65 70 75 80
Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
85 90 95
Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
100 105 110
Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
115 120 125
Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
130 135 140

<210> 38
<211> 173
<212> PRT
<213> Homo sapiens

<400> 38
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
1 5 10 15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
20 25 30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
35 40 45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
50 55 60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65 70 75 80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
85 90 95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
100 105 110

```
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
        115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Glu Val
    130                 135                 140
Cys Cys Ser Leu Arg Leu Ile Lys Gln Gln Arg Arg Asn Leu Ser Ser
145                 150                 155                 160
Pro Cys His Pro Ala Arg Arg Pro Val Leu Ser Pro Lys
                165                 170
```

<210> 39
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate polynucleotide sequence

<221> misc_feature
<222> (1)...(519)
<223> n = A,T,C or G

<400> 39

```
atggaytgyc argaraayga rtaytgggay cartggggnm gntgygtnac ntgycarmgn      60
tgyggnccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay     120
tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn     180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay     240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnyincar     300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty     360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn     420
gcnytngarg tntgytgyws nytnmgnytn athaarcarc armgnmgnaa yytnwsnwsn     480
ccntgycayc cngcnmgnmg nccngtnytn wsnccnaar                            519
```

<210> 40
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide ZC26463

<400> 40

```
atgcattaac cctcactaaa gggccttcct ggggctcttc ttcctct                    47
```

<210> 41
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide sequence ZC 26464

<400> 41
taatacgact cactataggg aggggcccct gctgctgttg tggtat 46

<210> 42
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC24670

<400> 42
atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca 49

<210> 43
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide sequence ZC 26471

<400> 43
taatacgact cactataggg aggcccccaa ggtctcagct ccagtat 47

<210> 44
<211> 657
<212> DNA
<213> murine

<400> 44
ggtggcatct ctcttccaat tggtctgatt gttggagtga catcactggg tctgctgatg 60
ttaggactgg tgaactgcat catcctggtg cagaggaaaa agaagccctc ctgcctacaa 120
agagatgcca aggtgcctca tgtgcctgat gagaaatccc aggatgcagt aggccttgag 180

cagcagcacc tgttgaccac agcacccagt tccagcagca gctccctaga gagctcagcc 240
agcgctgggg accgaagggc gccccctggg ggccatcccc aagcaagagt catggcggag 300
gcccaagggt ttcaggaggc ccgtgccagc tccaggattt cagattcttc ccacggaagc 360
cacgggaccc acgtcaacgt cacctgcatc gtgaacgtct gtagcagctc tgaccacagt 420
tctcagtgct cttcccaagc cagcgccaca gtgggagacc cagatgccaa gccctcagcg 480
tccccaaagg atgagcaggt ccccttctct caggaggagt gtccgtctca gtccccgtgt 540
gagactacag agacactgca gagccatgag aagcccttgc cccttggtgt gccggatatg 600
ggcatgaagc ccagccaagc tggctggttt gatcagattg cagtcaaagt ggcctga 657

<210> 45
<211> 824
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial cDNA sequence

<400> 45
ggtaccgaat tgtacgcgta tggggacttc ccatatcaat cagggacttt ccgctgggga 60
ctttccggtc tgactcatgc ttctgactca tgcttgggtg acatcatctc gactagtcgt 120
accttcccgt aaatccctcc ccttcccgga attacacacg cgtatttccc agaaaaggaa 180
ctgtagattt ctaggaattc aatccttggc cacgcgttta caccggaagt tttccatatt 240
aggaattcct tccggtttcc tttctcgagg ccaccgtggt tgagcccgac actcattcat 300
aaaacgcttg ttataaaagc agtggctgcg gcgccttcgt actccaaccg catctgcagc 360
gagcaactga gaagccaagg atccaggctg aattcatggg tctcaacccc cagctagttg 420
tcatcctgct cttctttctc gaatgtacca ggagccatat ccacggatgc gacaaaaatc 480
acttgagaga gatcatcggc attttgaacg aggtcacagg agaagggacg ccatgcacgg 540
agatggatgt gccaaacgtc ctcacagcaa cgaagaacac cacagagagt gagctcgtct 600
gtagggcttc caaggtgctt cgcatatttt atttaaaaca tgggaaaact ccatgcttga 660
agaagaactc tagtgttctc atggagctgc agagactctt tcgggctttt cgatgcctgg 720
attcatcgat aagctgcacc atgaatgagt ccaagtccac atcactgaaa gacttcctgg 780
aaagcctaaa gagcatcatg caaatggatt actcgtagtc taga 824

<210> 46
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide sequence ZC28835

<400> 46
taatacgact cactataggg aggcccccaa ggtctcagct ccagtat 47

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide sequence ZC 28836

<400> 47
gcaccggtgg cctcctgagg gggcact 27

<210> 48
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC 28830

<400> 48
gcaccggtgg catctctctt ccaattggt 29

<210> 49
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC 28837

<400> 49
gctctagagg ggtcaggcca ctttgactg 29

<210> 50
<211> 1081
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA construct

<400> 50

atggattgcc aagaaaatga gtactgggac caatggggac ggtgtgtcac ctgccaacgg 60
tgtggtcctg gacaggagct atccaaggat tgtggttatg gagagggtgg agatgcctac 120
tgcacagcct gccctcctcg caggtacaaa agcagctggg gccaccacaa atgtcagagt 180
tgcatcacct gtgctgtcat caatcgtgtt cagaaggtca actgcacagc tacctctaat 240
gctgtctgtg gggactgttt gcccaggttc taccgaaaga cacgcattgg aggcctgcag 300
gaccaagagt gcatcccgtg cacgaagcag acccccacct ctgaggttca atgtgccttc 360
cagttgagct tagtggaggc agatgcaccc acagtgcccc ctcaggaggt caccgttggc 420
atctctcttc caattggtct gattgttgga gtgacatcac tgggtctgct gatgttagga 480
ctggtgaact gcatcatcct ggtgcagagg aaaaagaagc cctcctgcct acaaagagat 540
gccaaggtgc ctcatgtgcc tgatgagaaa tcccaggatg cagtaggcct tgagcagcag 600
cacctgttga ccacagcacc cagttccagc agcagctccc tagagagctc agccagcgct 660
ggggaccgaa gggcgccccc tgggggccat ccccaagcaa gagtcatggc ggaggcccaa 720
gggtttcagg aggcccgtgc cagctccagg atttcagatt cttcccacgg aagccacggg 780
acccacgtca acgtcacctg catcgtgaac gtctgtagca gctctgacca cagttctcag 840
tgctcttccc aagccagcgc cacagtggga gacccagatg ccaagccctc agcgtcccca 900
aaggatgagc aggtcccctt ctctcaggag gagtgtccgt ctcagtcccc gtgtgagact 960
acagagacac tgcagagcca tgagaagccc ttgccccttg gtgtgccgga tatgggcatg 1020
aagcccagcc aagctggctg gtttgatcag attgcagtca aagtggcctg acccctctag 1080
a 1081